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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/767,597

DATE: 12/19/2001

TIME: 13:23:59

Input Set : N:\Crf3\RULE60\09767597.txt

Output Set: N:\CRF3\12192001\I767597.raw

3 <110> APPLICANT: Jegla, Timothy James
 4 ICAGEN, Inc.
 6 <120> TITLE OF INVENTION: Human HAC3
 8 <130> FILE REFERENCE: 018512-002210US
 10 <140> CURRENT APPLICATION NUMBER: 09/767,597
 11 <141> CURRENT FILING DATE: 2001-01-22
 13 <150> PRIOR APPLICATION NUMBER: 09/548,933
 14 <151> PRIOR FILING DATE: 2000-04-13
 16 <160> NUMBER OF SEQ ID NOS: 16
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 774
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: human hyperpolarization-activated voltage-gated
 27 cation channel 3 (HAC3)
 29 <400> SEQUENCE: 1
 30 Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr
 31 1 5 10 15
 33 Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala
 34 20 25 30
 36 Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His
 37 35 40 45
 39 Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val
 40 50 55 60
 42 Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser
 43 65 70 75 80
 45 Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp
 46 85 90 95
 48 Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro
 49 100 105 110
 51 Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val
 52 115 120 125
 54 Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn
 55 130 135 140
 57 Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala
 58 145 150 155 160
 60 Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp
 61 165 170 175
 63 Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu
 64 180 185 190
 66 Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
 67 195 200 205
 69 Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
 70 210 215 220
 72 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met

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73 225                230                235                240
75 Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly
76                245                250                255
78 Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
79                260                265                270
81 Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
82                275                280                285
84 Met Val Asn His Ser Trp Gly Arg Gln Tyr Ser His Ala Leu Phe Lys
85                290                295                300
87 Ala Met Ser His Met Leu Cys Ile Gly Tyr Gly Gln Gln Ala Pro Val
88 305                310                315                320
90 Gly Met Pro Asp Val Trp Leu Thr Met Leu Ser Met Ile Val Gly Ala
91                325                330                335
93 Thr Cys Tyr Ala Met Phe Ile Gly His Ala Thr Ala Leu Ile Gln Ser
94                340                345                350
96 Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu Lys Tyr Lys Gln Val Glu
97                355                360                365
99 Gln Tyr Met Ser Phe His Lys Leu Pro Ala Asp Thr Arg Gln Arg Ile
100                370                375                380
102 His Glu Tyr Tyr Glu His Arg Tyr Gln Gly Lys Met Phe Asp Glu Glu
103 385                390                395                400
105 Ser Ile Leu Gly Glu Leu Ser Glu Pro Leu Arg Glu Glu Ile Ile Asn
106                405                410                415
108 Phe Thr Cys Arg Gly Leu Val Ala His Met Pro Leu Phe Ala His Ala
109                420                425                430
111 Asp Pro Ser Phe Val Thr Ala Val Leu Thr Lys Leu Arg Phe Glu Val
112                435                440                445
114 Phe Gln Pro Gly Asp Leu Val Val Arg Glu Gly Ser Val Gly Arg Lys
115                450                455                460
117 Met Tyr Phe Ile Gln His Gly Leu Leu Ser Val Leu Ala Arg Gly Ala
118 465                470                475                480
120 Arg Asp Thr Arg Leu Thr Asp Gly Ser Tyr Phe Gly Glu Ile Cys Leu
121                485                490                495
123 Leu Thr Arg Gly Arg Arg Thr Ala Ser Val Arg Ala Asp Thr Tyr Cys
124                500                505                510
126 Arg Leu Tyr Ser Leu Ser Val Asp His Phe Asn Ala Val Leu Glu Glu
127                515                520                525
129 Phe Pro Met Met Arg Arg Ala Phe Glu Thr Val Ala Met Asp Arg Leu
130                530                535                540
132 Leu Arg Ile Gly Lys Lys Asn Ser Ile Leu Gln Arg Lys Arg Ser Glu
133 545                550                555                560
135 Pro Ser Pro Gly Ser Ser Gly Gly Ile Met Glu Gln His Leu Val Gln
136                565                570                575
138 His Asp Arg Asp Met Ala Arg Gly Val Arg Gly Arg Ala Pro Ser Thr
139                580                585                590
141 Gly Ala Gln Leu Ser Gly Lys Pro Val Leu Trp Glu Pro Leu Val His
142                595                600                605
144 Ala Pro Leu Gln Ala Ala Ala Val Thr Ser Asn Val Ala Ile Ala Leu
145                610                615                620

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147 Thr His Gln Arg Gly Pro Leu Pro Leu Ser Pro Asp Ser Pro Ala Thr
148 625                      630                      635                      640
150 Leu Leu Ala Arg Ser Ala Trp Arg Ser Ala Gly Ser Pro Ala Ser Pro
151                      645                      650                      655
153 Leu Val Pro Val Arg Ala Gly Pro Trp Ala Ser Thr Ser Arg Leu Pro
154                      660                      665                      670
156 Ala Pro Pro Ala Arg Thr Leu His Ala Ser Leu Ser Arg Ala Gly Arg
157                      675                      680                      685
159 Ser Gln Val Ser Leu Leu Gly Pro Pro Pro Gly Gly Gly Gly Arg Arg
160                      690                      695                      700
162 Leu Gly Pro Arg Gly Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro
163 705                      710                      715                      720
165 Gln Arg Ala Thr Gly Asp Gly Ser Pro Gly Arg Lys Gly Ser Gly Ser
166                      725                      730                      735
168 Glu Arg Leu Pro Pro Ser Gly Leu Leu Ala Lys Pro Pro Arg Thr Ala
169                      740                      745                      750
171 Gln Pro Pro Arg Pro Pro Val Pro Glu Pro Ala Thr Pro Arg Gly Leu
172                      755                      760                      765
174 Gln Leu Ser Ala Asn Met
175                      770
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 2325
180 <212> TYPE: DNA
181 <213> ORGANISM: Homo sapiens
182 <220> FEATURE:
183 <223> OTHER INFORMATION: human hyperpolarization-activated voltage-gated
184 cation channel 3 (HAC3)
185
187 <400> SEQUENCE: 2
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189 gcggtgcctc ccgttgctcc ccgcctgcg accgcggcct cagggtccgat ccccaaatct 120
190 gggcctgagc ctaagaggag gcaccttggg acgtctgtcc agcctacggt caacaagttc 180
191 tcccttcggg tgttcggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca 240
192 gcgggggcct ggatcatcca cccctacagc gacttccggt tttactggga cctgatcatg 300
193 ctgctgctga tgggtgggaa cctcatcgtc ctgcctgtgg gcacacctt cttcaaggag 360
194 gagaactccc cgccttggat cgtcttcaac gtattgtctg atactttctt cctactggat 420
195 ctggtgctca acttccgaac gggcatcggt gtggaggagg gtgctgagat cctgctggca 480
196 ccgcgggcca tccgcacgcg ctacctgcgc acatgggttc tgggtgacct catctcttct 540
197 atccctgtgg attacatctt cctagtgggt gagctggagc cacggttgga cgctgagggtc 600
198 tacaaaacgg cacgggccct acgcatcggt cgcttcacca agatccctaag cctgctgagg 660
199 ctgctccgcc tctccgcct catccgctac atacaccagt gggaggagat ctttcacatg 720
200 acctatgacc tggccagtgc tgtggttcgc atcttcaacc tcattgggat gatgctgctg 780
201 ctatgtcaact gggatggctg tctgcagttc ctggtgccca tgctgcagga cttccctccc 840
202 gactgctggg tctccatcaa ccacatggtg aaccactcgt ggggcccga gtattcccat 900
203 gccctgttca aggccatgag ccacatgctg tgcattggct atgggcagca ggcacctgta 960
204 ggcatgccg acgtctggct caccatgctc agcatgatcg taggtgccac atgctacgcc 1020
205 atgttcatcg gccatgccac ggcactcctc cagtcctcgg actcttcccg gcgtcagtac 1080
206 caggagaagt acaagcaggt ggagcagtac atgtccttcc acaagctgcc agcagacacg 1140
207 cggcagcgca tccacgagta ctatgagcac cgctaccagg gcaagatgtt cgatgaggaa 1200
208 agcatcctgg gcgagctgag cgagccgctt cgcgaggaga tcattaactt cacctgtcgg 1260

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209 ggctggtgg cccacatgcc gctgtttgcc catgccgacc ccagcttcgt cactgcagtt 1320
210 ctcaccaagc tgcgctttga ggtcttccag ccgggggatc tcgtggtgcg tgagggctcc 1380
211 gtggggagga agatgtactt catccagcat gggctgctca gtgtgctggc ccgcggcgcc 1440
212 cgggacacac gcctcaccga tggatcctac tttggggaga tctgcctgct aactaggggc 1500
213 cggcgacacag ccagtgttcg ggctgacacc tactgccgcc tttactcact cagcgtggac 1560
214 catttcaatg ctgtgcttga ggagttcccc atgatgcgcc gggcctttga gactgtggcc 1620
215 atggatcggc tgcctccgat cggcaagaag aattccatac tgcagcgga ggcctccgag 1680
216 ccaagtccag gcagcagtgg tggcatcatg gagcagcact tggtgcaaca tgacagagac 1740
217 atggctcggg gtgttcgggg tcgggcccc agcacaggag ctgagcttag tggaaagcca 1800
218 gtactgtggg agccactggg acatgcgcc cttcaggcag ctgctgtgac ctccaatgtg 1860
219 gccattgccc tgactcatca gcgggggccct ctgcccctct cccctgactc tccagccacc 1920
220 ctcttgctc gctctgcttg gcgctcagca ggctctccag cttccccgct ggtgcccgtc 1980
221 cgagctggcc catgggcac caccctccgc ctgcccgc caccctgccc aacctgcac 2040
222 gccagcctat cccgggcagg gcgctcccag gtctccctgc tgggtcccc tccaggagga 2100
223 ggtggacggc ggctaggacc tcggggccgc cactctcag cctcccaacc ctctctgcct 2160
224 cagcgggcaa caggcgatgg ctctcctggg cgtaagggat caggaagtga gcggctgcct 2220
225 ccctcagggc tcttgccaa acctccaagg acagcccagc ccccaggcc accagtgcct 2280
226 gagccagcca caccgcggg tctccagctt tctgccaaca tgtaa 2325
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230 <211> LENGTH: 24
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
236 primer
238 <400> SEQUENCE: 3
239 cagccatgga ggcagagcag cggc 24
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 28
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
249 primer
251 <400> SEQUENCE: 4
252 ggaggagatc tttcacatga catacgac 28
255 <210> SEQ ID NO: 5
256 <211> LENGTH: 24
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
262 primer
264 <400> SEQUENCE: 5
265 agtaggatcc atcggtgagg cgtg 24
268 <210> SEQ ID NO: 6
269 <211> LENGTH: 27
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence

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273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
275     primer
277 <400> SEQUENCE: 6
278 ttacatgttg gcagaaagct ggagacc 27
281 <210> SEQ ID NO: 7
282 <211> LENGTH: 29
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
288     amplification primer
290 <220> FEATURE:
291 <221> NAME/KEY: modified_base
292 <222> LOCATION: (24)
293 <223> OTHER INFORMATION: n = g, a, c or t
295 <400> SEQUENCE: 7
W--> 296 tgggaggaga tcttycayat gacntayga 29
299 <210> SEQ ID NO: 8
300 <211> LENGTH: 27
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
306     amplification primer
308 <220> FEATURE:
309 <221> NAME/KEY: modified_base
310 <222> LOCATION: (16)
311 <223> OTHER INFORMATION: n = g, a, c or t
313 <220> FEATURE:
314 <221> NAME/KEY: modified_base
315 <222> LOCATION: (25)
316 <223> OTHER INFORMATION: n = g, a, c or t
318 <400> SEQUENCE: 8
W--> 319 cgtctcgaat gcccknckca tcatngg 27
322 <210> SEQ ID NO: 9
323 <211> LENGTH: 26
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Description of Artificial Sequence:first round 5'
329     RACE gene specific primer
331 <400> SEQUENCE: 9
332 cctgctgccc atagccaatg cacagc 26
335 <210> SEQ ID NO: 10
336 <211> LENGTH: 25
337 <212> TYPE: DNA
338 <213> ORGANISM: Artificial Sequence
340 <220> FEATURE:

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/767,597

DATE: 12/19/2001

TIME: 13:24:00

Input Set : N:\Crf3\RULE60\09767597.txt

Output Set: N:\CRF3\12192001\I767597.raw

L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8